RID=1038413121-06030-900.

NCBI

results of BLAST

BLASTP 2.2.4 [Aug-26-2002]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.

RID: 1038413121-06030-16900

Query=
(10 letters)

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
1,243,428 sequences; 395,713,720 total letters

If you have any problems or questions with the results of this search
please refer to the **BLAST FAQs**

No significant similarity found. For reasons why, **click here**.

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
Posted date: Nov 25, 2002 10:56 PM
Number of letters in database: 395,713,720
Number of sequences in database: 1,243,428

Lambda   K   H
  0.321   0.134   0.465

Gapped
Lambda   K   H
  0.267   0.0410   0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 5,402,725
Number of Sequences: 1243428
Number of extensions: 76341
Number of successful extensions: 2
Number of sequences better than 10.0: 0
Number of HSP's better than 10.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 2
Number of HSP's gapped (non-prelim): 0
length of query: 10
length of database: 395,713,720
effective HSP length:
effective length of query: 24
effective length of database: 395,713,720

```
effective search space: 9497129280
effective search space used: 9497129280
T: 11
A: 40
X1: 16 ( 7.4 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.9 bits)
S2: 66 (30.0 bits)
```